



STIC Search Report

Biotech-Chem Library

File Copy
09/671,687
updated

STIC Database Tracking Number: 150771

TO: David Lamberston
Location: rem/2b79/2c70
Art Unit: 1636
Tuesday, April 19, 2005

Case Serial Number: 09/671687

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Lamberston,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



STIC-Biotech/ChemLib

150771

mg

From: Lambertson, David
Sent: Friday, April 15, 2005 10:25 AM
To: STIC-Biotech/ChemLib
Cc: Lambertson, David
Subject: Search Request

(STIC)

APR 15 2005

RECEIVED

Search Request

Examiner's Name:	David Lambertson
Examiner #:	79514
Art Unit:	1636
Room #:	02B79 Remsen
Mailbox room#:	02C70 Remsen
Phone:	(571) 272-0771
Results Format:	paper

Serial #:09/671687

Please Search:

Protein and Nucleic Acid databases for:

SEQ ID No: 3

Including:

1. Default Search.
2. Oligomer Search.
3. Interference Search.

Thanks,
Dave.

4/15/05
1-AA-028
1-AA-7NN
038

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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:14:54 ; Search time 73 Seconds

(without alignment)

5027.885 Million cell updates/sec

Title: US-09-671-687A-3

Perfect score: 5034

Sequence: 1 MSSGLWSQEKVTPWBERI.....RLLCDAYCMVQSPMTSLYK 949

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
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2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4983	99.0	953	7	ADC24816 Human bre
2	4983	99.0	953	8	ADQ95918 T cell ac
3	4980	99.0	960	8	ADR99244 DKFZp586D
4	4980	98.9	953	8	ADQ95916 T cell ac
5	4971.5	98.8	956	6	ABB82783 Human CYL
6	4971.5	98.8	956	8	ADR14489 Human NF-
7	4968.5	98.7	956	8	ADQ95920 T cell ac
8	3876.5	77.0	739	4	AAU23747 Novel hum
9	3862	76.7	731	3	RAY91954 Human cyt
10	3855	76.6	731	4	AB95828 Human pro
11	3636	72.2	685	4	RAM39254 Human pol
12	3563	70.8	698	4	RAM41040 Human pol
13	2755	54.7	558	4	AAU23211 Novel hum
14	2343	46.5	476	4	AB95719 Human pro
15	1275	25.3	261	5	ABB89233 Human pol
16	1173	23.3	238	5	ABB89234 Human pol
17	856	17.0	517	4	ABB61669 Drosophil
18	597	11.9	113	4	RAM14965 Peptide #
19	597	11.9	113	4	ABB33941 Peptide #
20	597	11.9	113	4	RAM27399 Peptide #
21	597	11.9	113	4	ABB28754 Peptide #
22	597	11.9	113	4	ABB19377 Peptide #
23	597	11.9	113	4	RAM67104 Human bon
24	597	11.9	113	4	RAM54704 Human bra
25	597	11.9	113	4	RAM02691 Peptide #

26	597	11.9	113	5	ABG36764 Human pep
27	568	11.3	106	8	ADK71947 Human ori
28	545	10.8	101	8	ADK71945 Human ori
29	514	10.2	96	8	ADK71949 Human ori
30	492	9.8	104	8	ADK71962 Human ori
31	491	9.8	91	8	ADK71943 Human ori
32	151	3.0	1392	2	AAV06999 Restin pr
33	151	3.0	1427	8	ADP56353 Human PRO
34	149	3.0	1427	2	AAAR10534 Human 160
35	146	2.9	354	7	ABM85235 Human pro
36	143	2.8	547	5	AAU74342 Human cyt
37	143	2.8	547	5	AB97353 Human hum
38	143	2.8	547	7	ADM04066 Human pro
39	139.5	2.8	1921	4	ABB62962 Drosophil
40	136	2.7	708	8	ADN99865 Novel hum
41	135.5	2.7	306	3	AAAB42642 Human ORP
42	135.5	2.7	306	7	ADB64836 Human pro
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44	135.5	2.7	721	8	ADI54654 Novel hum
45	135.5	2.7	2273	6	ABU38191 Protein e

ALIGNMENTS

RESULT 1

ADC24816
ID ADC24816 standard; protein; 953 AA.

XX AC ADC24816;

XX AC ADC24816;

DT 18-DEC-2003 (first entry)

XX Human breast specific polypeptide (BSP) DEX0238_137, SEQ ID NO:137.

DE Human breast specific polypeptide (BSP) DEX0238_137, SEQ ID NO:137.

XX Human; breast specific polypeptide; BSP; breast specific nucleic acid;

KW BSNAs; breast cancer; metastasis; non-cancerous disease; breast tissue;

KW identification; monitoring; diagnosis;

KW engineered breast tissue production; transgenic animal; drug screening;

KW cytostatic; gene therapy; vaccine; chromosome 16p13.3.

XX Homo sapiens.

OS Homo sapiens.

XX WO2003020900-A2.

FN 13-MAR-2003.

PD 13-MAR-2003.

XX 29-AUG-2002; 2002WO-US027777.

XX 31-AUG-2001; 2001US-0316306P.

XX (DIAD-) DIADEXUS INC.

XX Sun Y, Liu C, Salceda S;

XX WPI; 2003-290182/28.

XX N-PSDB; ADC24898.

XX New breast specific polypeptide useful for identifying, diagnosing,

XX monitoring, staging, imaging and treating breast cancer and non-cancerous

XX disease states in breast.

XX Disclosure; SEQ ID NO 137; 264pp; English.

XX The invention relates to breast specific polypeptides (BSPs) and nucleic

XX acids (breast specific nucleic acids; BSNAs) encoding them. The invention

XX also relates to vectors and host cells comprising a BSNAs sequence.

XX antibodies against BSPs; the recombinant production of BSPs; methods of

XX detection of BSNAs or BSPs in a sample; kits for detecting a risk of

XX cancer or presence of cancer in a patient; and vaccines comprising a BSNAs

XX or BSP. The invention additionally discloses fragments, mutants, fusion

XX proteins, homologous proteins and allelic variants of BSPs; methods for

XX identifying and designing agonists' and antagonists of BSPs; methods for

Result No.	Score	Query Match	Length	DB	ID	Description
1	151	3.0	1427	4	US-09-538-092-1044	Sequence 1044, Ap
2	135	2.7	1043	4	US-09-949-016-11650	Sequence 11650, A
3	130.5	2.6	184	4	US-09-248-796A-24175	Sequence 24175, A
4	125.5	2.5	1469	4	US-09-262-537-58	Sequence 58, Appl
5	118.5	2.4	1466	4	US-09-262-537-20	Sequence 20, Appl
6	118.5	2.4	1471	4	US-08-811-519-1	Sequence 1, Appl
7	118	2.3	267	3	US-09-399-913-57	Sequence 57, Appl
8	118	2.3	267	3	US-09-350-614-57	Sequence 57, Appl
9	118	2.3	677	4	US-09-270-767-45699	Sequence 45699, A
10	117	2.3	386	4	US-09-248-796A-17585	Sequence 17585, A
11	117	2.3	798	2	US-08-222-617A-8	Sequence 8, Appl
12	115.5	2.3	719	4	US-09-949-016-7766	Sequence 7766, Ap
13	114	2.3	523	4	US-09-248-796A-17555	Sequence 17555, A
14	114	2.3	850	4	US-09-129-603-2	Sequence 2, Appl
15	114	2.3	2777	4	US-10-220-587-4	Sequence 4, Appl
16	113	2.2	1226	1	US-08-280-443-2	Sequence 2, Appl
17	113	2.2	1226	1	US-08-457-459-2	Sequence 2, Appl
18	113	2.2	1226	1	US-08-555-678-2	Sequence 2, Appl
19	113	2.2	1226	5	PCM-US95-02275-2	Sequence 2, Appl
20	112.5	2.2	493	3	US-08-999-774A-12	Sequence 12, Appl
21	112.5	2.2	805	4	US-09-538-092-257	Sequence 257, App
22	112	2.2	734	4	US-09-328-352-4412	Sequence 4412, Ap
23	112	2.2	869	4	US-09-902-540-10125	Sequence 10125, A
24	111.5	2.2	1317	4	US-09-949-016-7588	Sequence 7588, Ap
25	110.5	2.2	657	3	US-09-370-368-7	Sequence 7, Appl
26	110	2.2	577	4	US-09-949-016-11572	Sequence 11572, A
27	109.5	2.2	868	4	US-09-538-092-787	Sequence 787, App

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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:25:00 ; Search time 97 Seconds
(without alignments)
3251.750 Million cell updates/sec

Title: US-09-671-687A-3
Perfect score: 5034
Sequence: 1 MSSGLWSQEKVTSFYWEERI.....RLLCDAYMCVQSPMTSLYK 949

Scoring table: BLOSUM62

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
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- 15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
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- 20: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4983	99.0	960	US-10-788-792-250	Sequence 250, App
2	4971.5	98.8	956	US-09-851-673-4	Sequence 4, Appli
3	4971.5	98.8	956	US-10-755-889-490	Sequence 490, App
4	3862	76.7	731	US-10-921-707-9	Sequence 9, Appli
5	1275	25.3	261	US-10-264-237-1609	Sequence 1609, Ap
6	1173	23.3	238	US-10-264-237-1610	Sequence 1610, Ap
7	597	11.9	113	US-09-864-761-34675	Sequence 34675, A
8	146	2.9	354	US-10-087-192-120	Sequence 120, App
9	143	2.8	547	US-10-108-260A-2751	Sequence 2751, Ap
10	143	2.8	547	US-10-275-595A-13	Sequence 13, Appli
11	135.5	2.7	306	US-10-104-047-2990	Sequence 2990, Ap
12	135.5	2.7	721	US-09-764-875-857	Sequence 857, App
13	135.5	2.7	2273	US-10-282-122A-66115	Sequence 66115, A

14	134.5	2.7	721	9	US-09-764-868-731	Sequence 731, App
15	134.5	2.7	721	11	US-09-764-875-1140	Sequence 1140, Ap
16	134.5	2.7	816	16	US-10-437-963-132799	Sequence 132799,
17	134	2.7	307	14	US-10-106-698-5606	Sequence 5606, Ap
18	133.5	2.7	1319	16	US-10-408-765A-343	Sequence 343, App
19	132.5	2.6	439	13	US-10-087-192-117	Sequence 117, App
20	130	2.6	717	15	US-10-369-493-22287	Sequence 22287, A
21	129.5	2.6	1281	16	US-10-363-829-373	Sequence 373, App
22	129.5	2.6	3298	14	US-10-160-758-16	Sequence 16, Appli
23	129.5	2.6	3298	14	US-10-174-677-8	Sequence 8, Appli
24	129.5	2.6	3298	15	US-10-120-801-51	Sequence 51, Appli
25	129.5	2.6	3298	15	US-10-210-172-50	Sequence 50, Appli
26	127.5	2.5	3217	15	US-10-311-623-8	Sequence 8, Appli
27	127	2.5	803	16	US-10-437-963-132702	Sequence 132702,
28	126.5	2.5	808	16	US-10-437-963-132681	Sequence 132681,
29	124	2.5	1474	14	US-10-225-567A-522	Sequence 522, App
30	124	2.5	1474	15	US-10-292-798-914	Sequence 914, App
31	124	2.5	2621	16	US-10-437-963-122168	Sequence 122168,
32	123.5	2.5	814	16	US-10-437-963-185098	Sequence 185098,
33	122.5	2.4	803	14	US-10-349-436-33	Sequence 33, Appli
34	122.5	2.4	892	15	US-10-276-774-1800	Sequence 1800, Ap
35	122.5	2.4	907	17	US-10-491-213-8	Sequence 8, Appli
36	122.5	2.4	1120	16	US-10-437-963-152821	Sequence 152821,
37	122.5	2.4	1282	16	US-10-437-963-110654	Sequence 110654,
38	122.5	2.4	1953	15	US-10-369-493-1945	Sequence 1945, Ap
39	122	2.4	2263	16	US-10-408-765A-2231	Sequence 2231, Ap
40	121	2.4	995	16	US-10-437-963-105117	Sequence 105117,
41	120.5	2.4	867	15	US-10-282-122A-57767	Sequence 57767, A
42	120.5	2.4	1033	9	US-09-888-615-75	Sequence 75, Appli
43	120.5	2.4	1109	15	US-10-425-114-72939	Sequence 72939, A
44	120.5	2.4	1471	10	US-09-998-027-4	Sequence 4, Appli
45	120.5	2.4	1471	14	US-10-165-099-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-10-788-792-250
; Sequence 250, Application US/10788792
; Publication No. US20040191819A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Pharmaceuticals Corporation
; APPLICANT: Eveleigh, Deepa
; APPLICANT: Bigwood, Douglas
; TITLE OF INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF USE
; FILE REFERENCE: 5152
; CURRENT APPLICATION NUMBER: US/10/788,792
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/450,655
; PRIOR FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 250
; LENGTH: 960
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-788-792-250

Query Match	99.0%	Score	4983	DB	16	Length	960
Best Local Similarity	99.5%	Pred. No.	0				
Mismatches	948	Conservative	0	Mismatches	1	Indels	4
Gaps							
Qy	1	MSSGLWSQEKVTSFYWEERIFVLLQLQSCVTDKOTKLLKVPKSGISGOYIDRSVGHSHRI	60				
Db	8	MSSGLWSQEKVTSFYWEERIFVLLQLQSCVTDKOTKLLKVPKSGISGOYIDRSVGHSHRI	67				
Qy	61	PSARKKNQIGLKILEQPHAVLFVDE-DVVEINEKFTLELLAITNCEERFSLFKNRRLS	119				
Db	68	PSARKKNQIGLKILEQPHAVLFVDEKDVVEINEKFTLELLAITNCEERFSLFKNRRLS	127				
Qy	120	KGLQIDVGCVPKVLQSGEBKFGVVRFPGLAERTVSGIFPGVELLEGGCGPTDGV	179				

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 18, 2005, 15:26:40 ; Search time 8972 Seconds
(without alignments)
5125.279 Million cell updates/sec

Title: US-09-671-687a-3

Perfect score: 5034

Sequence: 1 MSSGLNSQKVTSPYWEERI.....RLLCDAYMCYQSPYMSLYK 949

Scoring table:

BLOSUM62	Xgapop 10.0	Xgapext 0.5
	Ygapop 10.0	Ygapext 0.5
	Fgapop 6.0	Fgapext 7.0
	Delop 6.0	Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.spool_p/US09671687/runat 18042005.115018.17125/app query.fasta_1.1095
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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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Database :

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4: gb.om.*
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10: gb.ro.*
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14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	4983	99.0	3540	9	BC012342
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4	4980	98.9	3302	6	CQ834222

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6	4968.5	98.7	3311	6	CQ834226
7	4962	98.6	3480	6	CQ719792
8	4942	98.2	4527	6	BD231207
9	4718.5	93.7	4314	10	AK122389
10	4718.5	93.7	4501	10	BC042438
11	4712	93.6	3267	10	BC082001
12	4601	91.4	2845	6	BD160617
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31	1430.5	28.4	129025	2	AC145180
32	1370	27.2	1069	5	EX933038
33	1344	26.7	1335	5	EX934133
34	1262	25.1	837	6	BD149741
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ALIGNMENTS

RESULT 1
CQ834224
LOCUS CQ834224
DEFINITION Sequence 95 from Patent WO2004058805.
ACCESSION CQ834224
VERSION CQ834224.1 GI:50833761
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Matsuda A. and Yoneta, S.
TITLE T cell activating gene
JOURNAL Patent: WO 2004058805-A 95 15-JUL-2004;
Asahi Kasei Pharma Corporation (JP)
FEATURES
Location/Qualifiers
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linear PAT 29-JUL-2004

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 18, 2005, 15:25:35 ; Search time 1059 Seconds
(without alignments)
5304.848 Million cell updates/sec

Title: US-09-671-687A-3

Perfect score: 5034

Sequence: 1 MSSGLWQKVTSPYWERI.....RLLCDAYMCMQSPMTSLYK 949

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=N Geneseq.16Dec04 -QWTF=fastcap -SUFFIX=ring -MINMATCH=0.1 -LOOPCT=0
-LOOPTXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USBR=US09671687.cgn.1.708 @runat.18042005.115017.17115 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq.16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4983	99.0	3302	12 ADQ95917	Adq95917 T cell ac
2	4983	99.0	6831	10 ADC24898	Adc24898 Human bre
3	4980	98.9	3302	12 ADQ95915	Adq95915 T cell ac
4	4971.5	98.8	5371	10 ABV75394	Abv75394 Human CYL
5	4971.5	98.8	5371	13 ADR14488	Adri4488 Human NF-

6	4968.5	98.7	3311	12	ADQ95919	Adq95919 T cell ac
7	4942	98.2	4527	3	AAA08589	Aaa08589 Human cyt
8	4601	91.4	2845	4	AAH18625	Aah18625 Human cDN
9	3876.5	77.0	4716	4	AAAS41617	Aas41617 cDNA enco
10	3676	73.0	2523	4	AAI58410	Aai58410 Human pol
11	3676	73.0	2523	5	ADQ98620	Adq98620 DNA enco
12	3676	73.0	2523	9	ADB48380	Adb48380 Novel hum
13	3523	70.0	4286	4	AAI60196	Aai60196 Human pol
14	3329	66.1	2488	4	AAAS41081	Aas41081 cDNA enco
15	3022.5	60.0	2569	4	AAH18478	Aah18478 Human cDN
16	2468	49.0	2116	2	AAZ07515	Aaz07515 Human RAP
17	1778	35.3	1151	6	ABL89642	AbL89642 Human pol
18	1494	29.7	1013	6	ABL89643	AbL89643 Human pol
19	1490.5	29.6	1160	5	AAH05084	Aah05084 Human cDN
20	1262	25.1	837	4	AAH07749	Aah07749 Human cDN
21	1215	24.1	758	4	AAH05084	Aah05084 Human cDN
22	1102	21.9	617	6	ABQ60558	Abq60558 Human col
23	936	18.6	5433	4	ABL09704	AbL09704 Drosophil
24	879	17.5	557	6	ABQ60559	Abq60559 Human col
25	867.5	17.2	8990	4	AAK77783	Aak77783 Human imm
26	856	17.0	1655	4	ABL09705	AbL09705 Drosophil
27	626	12.4	376	8	ABX51704	Abx51704 Bovine ES
28	568	11.3	318	12	ADK71948	Adk71948 Human ori
29	545	10.8	303	12	ADK71946	Adk71946 Human ori
30	545	10.8	309	4	AAI20692	Aai20692 Probe #10
31	545	10.8	309	4	ABA65741	AbA65741 Human foe
32	545	10.8	309	4	AAI45907	Aai45907 Probe #14
33	545	10.8	309	4	ABA47848	AbA47848 Human bre
34	545	10.8	309	4	ABA32825	AbA32825 Probe #11
35	545	10.8	309	4	AAK39883	Aak39883 Human bon
36	545	10.8	309	4	AAK14143	Aak14143 Human bra
37	545	10.8	309	5	AAI06390	Aai06390 Probe #63
38	545	10.8	309	6	ABS13981	AbS13981 Human gen
39	514	10.2	288	12	ADK71950	Adk71950 Human ori
40	512	10.2	483	4	AAI11479	Aai11479 Probe #14
41	512	10.2	483	4	ABA53149	AbA53149 Human foe
42	512	10.2	483	4	AAI32754	Aai32754 Probe #14
43	512	10.2	483	4	ABA42721	AbA42721 Human bre
44	512	10.2	483	4	ABA22920	AbA22920 Probe #13
45	512	10.2	483	4	AAK26850	Aak26850 Human bon

ALIGNMENTS

RESULT 1
ADQ95917
ID ADQ95917 standard; cDNA; 3302 BP.
XX
AC ADQ95917;
XX
DT 07-OCT-2004 (first entry)
XX
DE T cell activation associated cDNA #48.
XX
KW ss; gene; antiallergic; antiarthritic; antiasthmatic; antidiabetic;
KW anti-HIV; antimicrobial; antirheumatic; immunosuppressive;
KW neuroprotective; gene therapy; T cell activation; diagnosis;
KW autoimmune disease; rheumatoid arthritis; asthma; multiple sclerosis;
KW diabetes; allergic disease; infectious disease; AIDS; chronic rejection;
KW organ; bone-marrow transplant.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT CDS 243..3104
FT /*tag= a
XX
XX WO2004058805-A2.
XX
XX 15-JUL-2004.
XX
XX 25-DEC-2003; 2003WO-JP016715.
XX

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 18, 2005, 15:33:50 ; Search time 376 Seconds
(without alignments)
4129.858 Million cell updates/sec

Title: US-09-671-687A-3

Perfect score: 5034

Sequence: 1 MSSGLWSQKVTSPYWEIRI.....RLLCDAYMCMYQSPWLSLYK 949

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=BIOSUM62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=spct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:
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3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2468	49.0	2116	4	US-09-646-403-3
3	185	3.7	110	4	US-09-513-999C-20085
4	151	3.0	5857	4	US-09-220-132-79
5	139	2.8	2825	4	US-09-949-016-1895
6	135	2.8	3130	4	US-09-949-016-5779
7	135	2.7	2643	3	US-09-399-913-56
8	133	2.7	2643	4	US-09-350-614-56
9	133	2.6	3245	4	US-09-774-528-352
10	130.5	2.6	1452	4	US-09-248-796A-10072
11	128.5	2.6	5610	4	US-09-262-537-57
12	126	2.5	1503	3	US-08-999-774A-11

13	126	2.5	4282	4	US-09-976-594-799	Sequence 799, App
14	126	2.5	4674	4	US-09-949-016-1717	Sequence 1717, App
15	122.5	2.4	1463	4	US-09-270-767-15085	Sequence 15085, A
c 16	122.5	2.4	31826	4	US-09-902-540-1256	Sequence 1256, App
c 17	121.5	2.4	13977	3	US-09-484-9708-60	Sequence 60, Appli
c 18	121.5	2.4	24333	4	US-09-639-207-9	Sequence 9, Appli
19	119.5	2.4	3545	3	US-08-885-291-54	Sequence 54, Appli
20	119.5	2.4	3545	3	US-09-496-672-54	Sequence 54, Appli
21	119.5	2.4	5715	3	US-09-107-847-1	Sequence 1, Appli
22	119	2.4	580073	4	US-08-545-528D-1	Sequence 1, Appli
23	118.5	2.4	5391	4	US-08-811-519-2	Sequence 2, Appli
24	118.5	2.4	5693	4	US-09-262-537-19	Sequence 19, Appli
25	118	2.3	1380	3	US-09-239-303-1	Sequence 1, Appli
26	118	2.3	2033	4	US-09-270-767-14130	Sequence 14130, A
27	118	2.3	2418	4	US-09-614-221A-495	Sequence 495, App
c 28	118	2.3	16047	4	US-09-902-540-1136	Sequence 1136, App
29	118	2.3	36820	4	US-09-949-016-16665	Sequence 16665, A
30	117.5	2.3	1794	4	US-09-949-016-2105	Sequence 2105, App
31	117.5	2.3	4926	2	US-08-853-310-1	Sequence 1, Appli
32	117	2.3	1158	4	US-09-248-796A-3462	Sequence 3462, App
33	117	2.3	2729	1	US-08-412-431-2	Sequence 2, Appli
34	117	2.3	2729	1	US-08-623-679-2	Sequence 2, Appli
35	117	2.3	2729	3	US-08-933-774-2	Sequence 2, Appli
36	117	2.3	2729	3	US-09-181-030-2	Sequence 2, Appli
37	117	2.3	2729	3	US-09-534-242-2	Sequence 2, Appli
38	117	2.3	2729	3	US-09-454-854-2	Sequence 2, Appli
39	117	2.3	2729	3	US-09-164-671-2	Sequence 2, Appli
40	117	2.3	2729	4	US-09-182-113-2	Sequence 2, Appli
41	117	2.3	2729	4	US-08-862-442-2	Sequence 2, Appli
c 42	116.5	2.3	1869	4	US-09-489-039A-3406	Sequence 3406, App
43	115.5	2.3	6671	1	US-08-280-443-1	Sequence 1, Appli
44	115.5	2.3	6671	1	US-08-457-459-1	Sequence 1, Appli
45	115.5	2.3	6671	1	US-08-555-678-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-620-312D-290
; Sequence 290, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyang
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunging
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 290
; LENGTH: 2523
; TYPE: DNA

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: April 18, 2005, 18:28:51 ; Search time 1146 Seconds
(without alignments)
5023.830 Million cell updates/sec

Title: US-09-671-687a-3
Perfect score: 5034
Sequence: 1 MSSGLWQKVTSPYWEERI.....RLLCDAYMCVMQSPMSLYK 949

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5622541 seqs, 303335566 residues
Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-MAXLEN=2000000000 -USER=US09671687 @CGN 1 1 723 @runat 18042005 115020 17247
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Database : Published Applications NA:**
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4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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22: /cgn2_6/ptodata/1/pubpna/US10J_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	4971.5	98.8	5371	10	US-09-851-673-3	Sequence 3, Appli
2	4971.5	98.8	5371	18	US-10-755-889-489	Sequence 489, App
3	4942	98.2	4527	18	US-10-921-707-25	Sequence 25, Appl
4	3676	73.0	2523	15	US-10-037-270-290	Sequence 290, App
5	3676	73.0	2523	17	US-10-117-722-290	Sequence 290, App
6	2468	49.0	2116	18	US-10-761-370-3	Sequence 3, Appli
C 7	1778	35.3	1151	17	US-10-264-237-204	Sequence 204, App
8	1494	29.7	1013	17	US-10-264-237-205	Sequence 205, App
C 9	1102	21.9	617	11	US-09-969-034-4253	Sequence 4253, Ap
C 10	879	17.5	557	11	US-09-969-034-4254	Sequence 4254, Ap
11	626	12.4	376	9	US-09-983-965-1633	Sequence 1633, Ap
C 12	545	10.8	309	9	US-09-864-761-18145	Sequence 18145, A
C 13	512	10.2	483	9	US-09-864-761-1386	Sequence 1386, Ap
14	412	8.2	425	10	US-09-918-995-35878	Sequence 35878, A
15	160.5	3.2	4847	17	US-10-152-319A-1764	Sequence 1764, Ap
16	151	3.0	5857	10	US-09-873-367C-305	Sequence 305, App
17	151	3.0	5857	19	US-10-843-641A-305	Sequence 305, App
18	148	2.9	3051	17	US-10-371-905A-3	Sequence 3, Appli
19	146	2.9	1380	13	US-10-087-192-119	Sequence 119, App
20	146	2.9	5563	18	US-10-723-860-1545	Sequence 1545, Ap
21	146	2.9	5607	18	US-10-723-860-5973	Sequence 5973, Ap
22	143	2.8	3287	17	US-10-275-595A-47	Sequence 47, Appl
23	143	2.8	3370	17	US-10-108-260A-308	Sequence 308, App
24	143	2.8	3592	10	US-09-814-353-20078	Sequence 20078, A
25	138	2.7	2154	17	US-10-369-493-45974	Sequence 45974, A
26	138	2.7	2451	18	US-10-437-963-30316	Sequence 30316, A
C 27	136.5	2.7	3409	18	US-10-723-860-6186	Sequence 6186, Ap
28	135.5	2.7	2618	17	US-10-104-047-1020	Sequence 1020, Ap
29	135.5	2.7	3103	11	US-09-764-875-259	Sequence 259, App
30	135.5	2.7	6822	17	US-10-282-122A-29931	Sequence 29931, A
31	135	2.7	2643	9	US-09-350-874-56	Sequence 56, Appl
32	135	2.7	2643	15	US-10-106-989-56	Sequence 56, Appl
33	134.5	2.7	3103	9	US-09-764-868-118	Sequence 118, App
34	134.5	2.7	3103	11	US-09-764-875-542	Sequence 542, App
35	134	2.7	1099	15	US-10-106-698-1329	Sequence 1329, App
36	134	2.7	2855	17	US-10-094-749-919	Sequence 919, App
37	133	2.6	3245	17	US-10-120-988-352	Sequence 352, App
38	132.5	2.6	1416	13	US-10-087-192-116	Sequence 116, App
39	132	2.6	3338	19	US-10-491-213-65	Sequence 65, Appl
40	130	2.6	2676	17	US-10-276-774-450	Sequence 450, App
41	129.5	2.6	4839	18	US-10-363-829-121	Sequence 121, App
42	129.5	2.6	10531	14	US-10-160-758-10	Sequence 10, Appl
43	129.5	2.6	10759	17	US-10-210-172-49	Sequence 49, Appl
44	128.5	2.6	2446	9	US-09-801-275-1	Sequence 1, Appli
45	128.5	2.6	2446	16	US-10-170-789-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-09-851-673-3
; Sequence 3, Application US/09851673
; Publication No. US20030165985A1
; GENERAL INFORMATION:
; APPLICANT: Derry, Jonathan
; APPLICANT: Fanslow, William
; APPLICANT: Dougall, William
; TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS OR ANTAGONISTS OF CD40 SIGNALING
; FILE REFERENCE: 3198
; CURRENT APPLICATION NUMBER: US/09/851,673
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5371
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:18:59 ; Search time 22 Seconds
(without alignments)
4150.441 Million cell updates/sec

Title: US-09-671-687A-3

Perfect score: 5034

Sequence: 1 MSGLWSQKVTSPYWEERI.....RLLCDAYMCYQSPMSLYK 949

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	613.5	12.2	1021	2 F88568	protein F40F12.5 [
2	590.5	11.7	727	2 S42334	F40F12.5 protein -
3	151	3.0	1352	2 A43336	microtubule-vesicl
4	151	3.0	1427	2 S22595	restin - human
5	149.5	3.0	1046	2 T42734	cytoplasmic linker
6	149	3.0	1046	2 T42720	cytoplasmic linker
7	135.5	2.7	2273	2 T09083	hemagglutinin/hemo
8	130	2.6	717	2 S38177	SSV7 protein homol
9	125.5	2.5	1921	2 T13827	kinesin-73 - fruit
10	124.5	2.5	1146	2 F83853	5-methyltetrahydro
11	124	2.5	3624	2 AD0835	large repetitive p
12	122.5	2.4	1953	2 S63244	BNI1 protein - yea
13	122	2.4	1791	2 T02345	hypothetical prote
14	121	2.4	1498	2 E86302	hypothetical prote
15	121	2.4	1641	2 T10955	early nodulin bind
16	120	2.4	499	2 S56265	hypothetical prote
17	119	2.4	662	2 T18233	probable transcrip
18	118.5	2.4	1466	2 T17138	CuIAB protein - ra
19	118.5	2.4	1467	2 T18411	latrophilin-1, bra
20	118.5	2.4	1471	2 T17149	CuIAB protein - ra
21	118.5	2.4	1472	2 T18413	latrophilin-1, bra
22	118.5	2.4	1510	2 T17145	CuIAB protein - ra
23	118.5	2.4	1515	2 T17156	CuIAB protein - ra
24	116.5	2.3	825	2 T47164	hypothetical prote
25	116.5	2.3	2484	2 T26216	hypothetical prote
26	116.5	2.3	2607	2 T26215	hypothetical prote
27	115.5	2.3	514	2 T25509	hypothetical prote
28	115.5	2.3	670	2 T38446	microtubule-associ
29	115.5	2.3	673	2 S35335	transcription fact

30 115.5 2.3 1341 2 T17285 hypothetical prote
31 115 2.3 471 2 S57591 hypothetical prote
32 114.5 2.3 752 2 D96699 DNA polymerase III
33 114.5 2.3 1161 2 B70387 probable membrane
34 114.5 2.3 1357 2 S61187 ubiquitin carboxyl
35 114 2.3 438 2 T39772 hypothetical prote
36 114 2.3 739 2 T15215 protein K09H1.1
37 113.5 2.3 974 2 D89057 racGAP protein - s
38 113.5 2.3 1335 2 T18289 protein F21H11.2
39 113.5 2.3 2700 2 D88450 probable RNA-bindin
40 113 2.2 753 2 A96747 adenosine deaminas
41 113 2.2 1226 1 S65593 phaseolin G-box bi
42 112.5 2.2 642 2 T10861 ubiquitin-specific
43 112.5 2.2 805 2 S50277 gene X104 protein
44 112.5 2.2 1116 2 I54378 dystrophin, muscle
45 112 2.2 3685 1 A27605

ALIGNMENTS

RESULT 1

P88568

Protein F40F12.5 [imported] - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001

C/Accession: F88568

R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo
A/Reference number: A75000; MUID:99069613; PMID:9851916

A/Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C.el

A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an

A/Accession: F88568

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1021 <STO>

A/Cross-references: GB:chr_III; PIDN:CAA82939.1; PID:g3877002; GSPDB:GN00021; CESP:F40F

C/Genetics:

A/Gene: F40F12.5

A/Map position: 3

Query Match 12.2%; Score 613.5; DB 2; Length 1021;
Best Local Similarity 23.7%; Pred. No. 4.6e-34;
Matches 256; Conservative 154; Mismatches 315; Indels 357; Gaps 46;

Qy 103 TNCERFSLP-----KNRNLKGLQIDVGCYKVKQLRSGEEKPPGVVRRFGLLAERTV 157
Db 43 TQSEKSNLYTSENTSNRLNLNQNIPVGT----- 73

Qy 158 SGIFFGVLEEGRCOGFTDGVYQKQLFQCDGCFVALDKLELIEDDDTALE----- 211
Db 74 --LIDGFELINEASGSGFLD-----DQL-----VDVSDYSRDRTKLDRNRNSP 115

Qy 212 -----SDYAGDGTQWVELPPLLEI-----NSRVS 235
Db 116 ELIVALLQKVGQIRSSNYGREGEEPCVHIPTGVWREADDKMSKELKEWFTKGRAS 175

Qy 236 --LKGG-----ETIESGTVIFC-----DVLPGKESLGYFVGVMDMNPIGNWDGRPDGV 281
Db 176 SHLRDGLAMPMBELDC--TPLICAMITRSDVMRNQDAIHLLAVSVBKRI-----EV 226

Qy 282 LCSFACVESTILLHINDIIPESV--TQERRPPKLAWSRGVCGKG----- 324
Db 227 YQNFWFNFILNLKIGDSVSEVDETMRRYPAKVSIGERPEASGIWYVNDPQNTSOWP 286

Qy 325 -----SSGHNKP-----KATGSTS--DPCNRRSELYFTLN-----GSSVDS-- 358
Db 287 SSNQSYSSSHDLNRQFDTNWFMFGSGSSVAFSN--SRLYYSPNQMHMPKMGGSVALY 344

Qy 359 -----QPQSKSKNTWYIDEVABDPKASLTETIS 385
Db 345 DNRRLVQYSGDEQYRSAPKAPRERIIPVSRQOQTEIQRN-----SRSMKPSE 393

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 18, 2005, 15:32:50 ; Search time 6177 Seconds

(without alignments)
5847.983 Million cell updates/sec

Title:

Perfect score: 5034

Sequence: 1 MSSGLWQKVTSPYWEERI.....RLLCDAYMCYQSPMSLYK 949

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q/cgn2 1/USPTO spool p/US09671687/runat 18042005 115018 17139/app_query.fasta_1.1095
-DB=EST -OPMT=fastcap -SUPFIX=rat -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09671687 @CGN 1 1 5180 @runat 18042005 115018 17139 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gest1.*
9: gb_gest2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4494	89.3	3496	3 AF161542	AF161542 Homo sapi
2	4313	85.7	2862	9 AY406374	AY406374 Homo sapi
3	4102	81.5	2730	9 AY406376	AY406376 Mus muscu
4	3768	74.9	2862	9 AY406375	AY406375 Pan trogl
5	2952	58.6	2220	3 AK039054	AK039054 Mus muscu
6	2769	55.0	3137	3 BC028885	BC028885 Mus muscu
7	1572.5	31.2	1063	5 BQ433523	BQ433523 AGENCOURT
8	1570	31.2	1039	4 BM457960	BM457960 AGENCOURT
9	1459.5	29.0	1478	3 AK042764	AK042764 Mus muscu

10	1435	28.5	938	4 BI666276	BI666276
11	1426	28.3	2218	3 AK048183	AK048183 Mus muscu
12	1416.5	28.1	1133	4 BM480127	BM480127 AGENCOURT
13	1384	27.5	812	6 CA512526	CA512526 UI-R-FJO-
14	1363	27.1	1892	3 BC024596	BC024596 Mus muscu
15	1340	26.6	837	4 BG867631	BG867631 602787414
16	1302	25.9	816	5 BQ442079	BQ442079 UI-M-EXO-
17	1288	25.6	721	5 BP162259	BP162259 BP162259
18	1286.5	25.6	889	5 BU505487	BU505487 AGENCOURT
19	1280	25.4	783	4 BM016881	BM016881 603643383
20	1268.5	25.2	715	7 CN157036	CN157036 944487 MA
21	1267.5	25.2	840	5 BP144628	BP144628 BP144628
22	1262	25.1	837	1 AU137267	AU137267 AU137267
23	1233	24.5	726	7 CR772310	CR772310 DKFZp468L
24	1233	24.5	717	7 CF750356	CF750356 UI-M-HJO-
25	1215	24.1	758	1 AU122742	AU122742 AU122742
26	1202.5	23.9	791	7 CN461343	CN461343 UI-M-HNO-
27	1198	23.8	743	6 CD351332	CD351332 UI-M-GIO-
28	1170	23.2	677	6 CD628856	CD628856 560768370
29	1165	23.1	648	1 AL707441	AL707441 DKFZp686M
30	1165	23.1	697	4 BM724143	BM724143 UI-E-EOI-
31	1160.5	23.1	781	7 CK636353	CK636353 UI-M-HNO-
32	1158	23.0	826	7 CK597829	CK597829 AGENCOURT
33	1152	22.9	708	6 CB466941	CB466941 732655 MA
34	1152	22.9	794	2 BF141863	BF141863 601791346
35	1151	22.9	770	4 BI906770	BI906770 603064511
36	1139.5	22.6	785	6 CB235676	CB235676 AGENCOURT
37	1128	22.4	906	5 BU461394	BU461394 603774393
38	1127.5	22.4	907	5 BQ438227	BQ438227 AGENCOURT
39	1118	22.2	702	2 BB648023	BB648023 BB648023
40	1117.5	22.2	755	7 CO404877	CO404877 AGENCOURT
41	1107.5	22.0	723	6 CD559213	CD559213 AGENCOURT
42	1105.5	22.0	1134	5 BM904688	BM904688 AGENCOURT
43	1102	21.9	637	2 AW985722	AW985722 Uf85b05.Y
44	1094	21.7	639	7 CN704295	CN704295 E0485H10-
45	1092.5	21.7	1365	3 AY383658	AY383658 Rattus no

ALIGNMENTS

RESULT 1
AF161542
LOCUS AF161542 3496 bp mRNA linear HTC 22-MAY-2001
DEFINITION Homo sapiens HSPC057 mRNA, complete cds.
ACCESSION AF161542
VERSION AF161542.1 GI:6841351
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3496)
Zhang, Q.H., Ye, M., Wu, X.Y., Ren, S.X., Zhao, C.J., Fu, G.,
Shen, Y., Fan, H.Y., Lu, G., Zhong, M., Xu, X.R., Han, Z.G., Zhang, J.W.,
Tao, J., Huang, Q.H., Zhou, J., Hu, G.X., Gu, J., Chen, S.J. and Chen, Z.
Cloning and functional analysis of cDNAs with open reading frames
for 300 previously undefined genes expressed in CD34+ hematopoietic
stem/progenitor cells
Genome Res. 10 (10), 1546-1560 (2000)

JOURNAL MEDLINE
20499367
11042152
PUBMED
REFERENCE 2 (bases 1 to 3496)
Zhang, Q.H., Ye, M., Zhou, J., Shen, Y., Wu, X.Y., Guan, Z.Q., Wang, L.,
Fan, H.Y., Mao, Y.F., Dai, M., Huang, Q.H., Chen, S.J. and Chen, Z.
Human full length cDNA cloned from cd34+ stem cells
Unpublished
REFERENCE 3 (bases 1 to 3496)
Zhang, Q.H., Ye, M., Zhou, J., Shen, Y., Wu, X.Y., Guan, Z.Q., Wang, L.,
Fan, H.Y., Mao, Y.F., Dai, M., Huang, Q.H., Chen, S.J. and Chen, Z.
Direct Submission
Submitted (14-MAY-1999) Shanghai Institute of Hematology, Shanghai
Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II,
Shanghai 200025, P. R. China

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:16:44 ; Search time 65 Seconds
(without alignments)
7476.356 Million cell updates/sec

Title: US-09-671-687A-3

Perfect score: 5034

Sequence: 1 MSSGLWSQEKVTSFYWEERI.....RLLCDAYMCVQSPMTSLYK 949

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4971.5	98.8	956	1	CYLD HUMAN
2	4718.5	93.7	952	1	CYLD MOUSE
3	4712	93.6	953	2	Q66H62
4	1207	24.0	778	2	Q7Q414
5	1136.5	22.6	551	2	Q8IPC3
6	1136.5	22.6	639	2	Q8IPC5
7	1134	22.5	550	2	Q8IPC4
8	1132.5	22.5	639	2	Q8IFY0
9	1092.5	21.7	454	2	Q6TXJ6
10	856	17.0	517	2	Q9VL04
11	619	12.3	1144	2	Q7JMS4
12	183.5	3.6	258	2	Q7PJA3
13	153.5	3.0	528	2	Q6BU87
14	151	3.0	653	2	Q6P529
15	149.5	3.0	1046	1	REST HUMAN
16	149.5	3.0	1046	2	O55156
17	149	3.0	1046	2	Q9Z0H8
18	147.5	2.9	449	2	Q86WU4
19	146	2.9	350	2	Q6PIA3
20	145	2.9	547	2	Q96DZ5
21	145	2.9	1556	2	Q9VRF1
22	143.5	2.9	495	2	Q6FM69
23	143.5	2.9	1047	2	Q9EP81
24	143	2.8	547	2	Q8WU11
25	142.5	2.8	1606	2	Q7PVQ8
26	142	2.8	1012	2	Q7TS19
27	141	2.8	1012	2	Q8CHU1
28	141	2.8	1429	2	Q6DP6E
29	140.5	2.8	429	2	Q96C99
30	140	2.8	924	2	Q7VDY2
31	139.5	2.8	1921	2	Q86BR0

ALIGNMENTS

RESULT 1

ID	CYLD HUMAN	STANDARD;	PRT;	956 AA.
AC	Q9NOC7; Q94934; Q7L3N6; Q96EH0; Q9NZX9;			
DT	25-OCT-2004 (Rel. 45, Created)			
DT	25-OCT-2004 (Rel. 45, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Probable ubiquitin carboxyl-terminal hydrolase CYLD (EC 3.1.2.15)			
DE	(Ubiquitin thiolesterase CYLD) (Ubiquitin-specific processing protease CYLD) (Deubiquitinating enzyme CYLD) (HSPC057).			
GN	Name-CYLD; Synonyms-CYLD1, KIAA0849;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]				
RP	SEQUENCE FROM N.A. (ISOFORM 1), DISEASE, AND TISSUE SPECIFICITY.			
RX	MEDLINE=20296617; PubMed=10835629; DOI=10.1038/76006;			
RA	Bignell G.R., Brown C., Biggs P.J., Lakhani S.R., Jones C., Hansen J., Blair E., Hofmann B., Siebert R., Turner G., Evans D.G., Schlander-Stumpel C., Beemer F.A., Van Den Ouweland A., Halley D., Delpech B., Cleveland M.G., Leigh I., Leisti J., Rasmussen S., Wallace M.R., Fenske C., Banerjee P., Oiso N., Chaggar R., Merrett S., Leonard N., Huber M., Hohl D., Chapman P., Burn J., Swift S., Smith A., Ashworth A., Stratton M.R.;			
RT	"Identification of the familial cylindromatosis tumor suppressor gene."			
RL	Nat. Genet. 25:160-165 (2000).			
RN	[2].			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	TISSUE=Brain;			
RX	MEDLINE=99156230; PubMed=10048485;			
RA	Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosewa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;			
RT	"Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."			
RL	DNA Res. 5:355-364 (1998).			
RN	[3].			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	TISSUE=Uterus;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,			

32	139	2.8	446	2	Q757P1
33	138.5	2.8	1172	2	Q7RF04
34	138.5	2.8	1937	2	Q6A062
35	138	2.7	724	2	Q8BWD1
36	138	2.7	1024	2	O14527
37	138	2.7	1391	2	Q922J3
38	137.5	2.7	992	2	Q6CIK8
39	137	2.7	868	2	Q9SDN6
40	136.5	2.7	359	2	Q7PVQ6
41	136	2.7	887	2	Q6FQF0
42	135.5	2.7	2273	2	O31152
43	135.5	2.7	2273	2	Q7DDH8
44	135	2.7	1046	2	Q9UDT6
45	134.5	2.7	657	2	Q7Z3N8

Q757P1	ashbya goes
Q7RF04	plasmodium
Q6A062	mus musculus
Q8BWD1	mus musculus
O14527	homo sapien
Q922J3	mus musculus
Q6CIK8	yarrowia li
Q9SDN6	nicotiana t
Q7PVQ6	anopheles g
Q6FQF0	candida gla
O31152	neisseria m
Q7DDH8	neisseria m
Q9UDT6	homo sapien
Q7Z3N8	homo sapien